David E Kim

List of Publications by Citations

31 papers	5,366 citations	25 h-index	32 g-index
32 ext. papers	6,361 ext. citations	7.7 avg, IF	5.32 L-index

#	Paper	IF	Citations
31	Protein structure prediction and analysis using the Robetta server. *Nucleic Acids Research*, **2004**, 32, W526-31	10.1	1239
30	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. *Methods in Enzymology*, **2011**, 487, 545-74	1.7	1216
29	Computational alanine scanning of protein-protein interfaces. *Science Signaling*, **2004**, 2004, pl2	8.8	361
28	Protein structure determination using metagenome sequence data. *Science*, **2017**, 355, 294-298	33.3	346
27	Automated prediction of CASP-5 structures using the Robetta server. *Proteins: Structure, Function and Bioinformatics*, **2003**, 53 Suppl 6, 524-33	4.2	241
26	A breakdown of symmetry in the folding transition state of protein L. *Journal of Molecular Biology*, **2000**, 298, 971-84	6.5	210
25	Simultaneous Optimization of Biomolecular Energy Functions on Features from Small Molecules and Macromolecules. *Journal of Chemical Theory and Computation*, **2016**, 12, 6201-6212	6.4	199
24	Large-scale determination of previously unsolved protein structures using evolutionary information. *ELife*, **2015**, 4, e09248	8.9	173
23	Structure prediction for CASP7 targets using extensive all-atom refinement with Rosetta@home. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69 Suppl 8, 118-28	4.2	158
22	Physically realistic homology models built with ROSETTA can be more accurate than their templates. *Proceedings of the National Academy of Sciences of the United States of America*, **2006**, 103, 5361-6	11.5	138
21	Free modeling with Rosetta in CASP6. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61 Suppl 7, 128-34	4.2	117
20	Prediction of CASP6 structures using automated Robetta protocols. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61 Suppl 7, 157-66	4.2	114
19	Comprehensive computational design of ordered peptide macrocycles. *Science*, **2017**, 358, 1461-1466	33.3	96
18	Improved de novo structure prediction in CASP11 by incorporating coevolution information into Rosetta. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 67-75	4.2	82
17	Sampling bottlenecks in de novo protein structure prediction. *Journal of Molecular Biology*, **2009**, 393, 249-60	6.5	80
16	Automated prediction of domain boundaries in CASP6 targets using Ginzu and RosettaDOM. *Proteins: Structure, Function and Bioinformatics*, **2005**, 61 Suppl 7, 193-200	4.2	72
15	One contact for every twelve residues allows robust and accurate topology-level protein structure modeling. *Proteins: Structure, Function and Bioinformatics*, **2014**, 82 Suppl 2, 208-18	4.2	70

List of Publications

14	Accurate computer-based design of a new backbone conformation in the second turn of protein L. *Journal of Molecular Biology*, **2002**, 315, 471-7	6.5	70
13	Protein structure prediction using Rosetta in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 113-121	4.2	63
12	Structures of the B1 domain of protein L from Peptostreptococcus magnus with a tyrosine to tryptophan substitution. *Acta Crystallographica Section D: Biological Crystallography*, **2001**, 57, 480-7		54
11	Single-site mutations induce 3D domain swapping in the B1 domain of protein L from Peptostreptococcus magnus. *Structure*, **2001**, 9, 1017-27	5.2	50
10	Protein homology model refinement by large-scale energy optimization. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 3054-3059	11.5	49
9	The single helix in protein L is largely disrupted at the rate-limiting step in folding. *Journal of Molecular Biology*, **1998**, 284, 807-15	6.5	49
8	Automatic structure prediction of oligomeric assemblies using Robetta in CASP12. *Proteins: Structure, Function and Bioinformatics*, **2018**, 86 Suppl 1, 283-291	4.2	29
7	High-accuracy refinement using Rosetta in CASP13. *Proteins: Structure, Function and Bioinformatics*, **2019**, 87, 1276-1282	4.2	26
6	Contributions of amino acid side chains to the kinetics and thermodynamics of the bivalent binding of protein L to Ig kappa light chain. *Biochemistry*, **2004**, 43, 2445-57	3.2	20
5	An analysis and evaluation of the WeFold collaborative for protein structure prediction and its pipelines in CASP11 and CASP12. *Scientific Reports*, **2018**, 8, 9939	4.9	16
4	Structure prediction using sparse simulated NOE restraints with Rosetta in CASP11. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84 Suppl 1, 181-8	4.2	11
3	Protein tertiary structure prediction and refinement using deep learning and Rosetta in CASP14. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 1722-1733	4.2	9
2	Crystallization and preliminary X-ray diffraction studies of mutants of B1 IgG-binding domain of protein L from Peptostreptococcus magnus. *Acta Crystallographica Section D: Biological Crystallography*, **2000**, 56, 506-8		4
1	Protein sequence design by explicit energy landscape optimization		4